

SEQUENCE LISTING

<110> Ruan, Yong-Ling
Furbank, Robert T.
Danny, Llewellyn J.

<120> Modification of sucrose synthase gene expression in plant tissue and uses therefor

<130> GHSUSY WO1

<150> 60/251852

<151> 2000-12-08

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 2625

<212> DNA

<213> Gossypium hirsutum

<220>

<221> misc_feature

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<223> n = any nucleotide (a,g,c,t)

<220>

<221> CDS

<222> (1)..(2625)

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Met Ala Glu Arg Ala Leu Thr Arg Val His Ser Leu Arg Glu Arg Leu	
1 5 10 15	

gat gag acc ctt ctt gct cac agg aac gag att ttg gcc ttg ctc tca	96
Asp Glu Thr Leu Leu Ala His Arg Asn Glu Ile Leu Ala Leu Leu Ser	
20 25 30	

agg atc gag ggc aaa gga aaa gga att ctg caa cac cat caa att att	144
Arg Ile Glu Gly Lys Gly Lys Gly Ile Leu Gln His His Gln Ile Ile	
35 40 45	

cta gag ttt gaa gct atc cct gaa gag aac aga aag aag ctc gct aat	192
Leu Glu Phe Glu Ala Ile Pro Glu Glu Asn Arg Lys Lys Leu Ala Asn	
50 55 60	

ggg gca ttt ttt gaa gta ttg aag gct agt cag gaa gcg atc gtg ttg	240
Gly Ala Phe Phe Glu Val Leu Lys Ala Ser Gln Glu Ala Ile Val Leu	
65 70 75 80	

cct cca tgg gtt gca ctt gct gtt cgt cca agg cct ggt gtt tgg gag	288
Pro Pro Trp Val Ala Leu Ala Val Arg Pro Arg Pro Gly Val Trp Glu	

	85	90	95	
	tac att aga gtg aat gtt cac gcc ctt gtt gtt gag gaa ctc act gtt			336
	Tyr Ile Arg Val Asn Val His Ala Leu Val Val Glu Glu Leu Thr Val			
	100	105	110	
	gct gag tat ctc cac ttc aag gaa gag ctt gtt gat gga agt tca aat			384
	Ala Glu Tyr Leu His Phe Lys Glu Glu Leu Val Asp Gly Ser Ser Asn			
	115	120	125	
	gga aac ttt gtt ttg gaa ttg gat ttt gag ccc ttc aac tca tca ttc			432
	Gly Asn Phe Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ser Ser Phe			
	130	135	140	
	ccc cgc cca act ctt tca aaa tcc att ggt aat ggt gtg gag ttc cta			480
	Pro Arg Pro Thr Leu Ser Lys Ser Ile Gly Asn Gly Val Glu Phe Leu			
	145	150	155	160
	aat cgt cac ctt tcg gca aaa ttg ttc cat gac aag gag agc atg cac			528
	Asn Arg His Leu Ser Ala Lys Leu Phe His Asp Lys Glu Ser Met His			
	165	170	175	
	ctt ttg ctc gaa ttc ctc aga gtc cat tgt cac aag ggc aag aac atg			576
	Pro Leu Leu Glu Phe Leu Arg Val His Cys His Lys Gly Lys Asn Met			
	180	185	190	
	atg ttg aat gac aga att cag aac ttg aat gct ctt caa cat gtt ttg			624
	Met Leu Asn Asp Arg Ile Gln Asn Leu Asn Ala Leu Gln His Val Leu			
	195	200	205	
	agg aaa gca gag gag tat ctt ggt acc cta cct cct gag aca cca tgt			672
	Arg Lys Ala Glu Glu Tyr Leu Gly Thr Leu Pro Pro Glu Thr Pro Cys			
	210	215	220	
	gcc gaa ttc gaa cac cgg ttc cag gaa atc ggt ttg gaa aga ggt tgg			720
	Ala Glu Phe Glu His Arg Phe Gln Glu Ile Gly Leu Glu Arg Gly Trp			
	225	230	235	240
	ggt gac acc gca gaa cgc gtg ctc gag atg atc caa ctc ctt ttg gat			768
	Gly Asp Thr Ala Glu Arg Val Leu Glu Met Ile Gln Leu Leu Leu Asp			
	245	250	255	
	ctt ctt gag gca act gat cct tgc acc ctt gag aag ttc ctt ggg aga			816
	Leu Leu Glu Ala Thr Asp Pro Cys Thr Leu Glu Lys Phe Leu Gly Arg			
	260	265	270	
	atc ccc atg gtg ttc aat gtt gtg att ctc act ccc cac gga tac ttc			864
	Ile Pro Met Val Phe Asn Val Val Ile Leu Thr Pro His Gly Tyr Phe			
	275	280	285	
	gct caa gac aat gtt ttg ggg tat ccc gac acc ggt ggg cag gtt gtt			912
	Ala Gln Asp Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val			
	290	295	300	
	tac atc ttg gat caa gtc cga gct ttg gag aat gag atg ctc ctc cgt			960
	Tyr Ile Leu Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg			
	305	310	315	320

ata aag caa caa gga ctc aac atc acc cct cga atc ctc att att act	1008
Ile Lys Gln Gln Gly Leu Asn Ile Thr Pro Arg Ile Leu Ile Ile Thr	
325 330 335	
aga ctt ctt cct gat gct gtc gga aca aca tgc ggt caa cga ctt gag	1056
Arg Leu Leu Pro Asp Ala Val Gly Thr Thr Cys Gly Gln Arg Leu Glu	
340 345 350	
aaa gta tac gga aca gag cac tcg gat att ctt cga gta ccc ttc aga	1104
Lys Val Tyr Gly Thr Glu His Ser Asp Ile Leu Arg Val Pro Phe Arg	
355 360 365	
aca gaa aag gga att gtt cga aaa tgg atc tca aga ttt gaa aaa gtc	1152
Thr Glu Lys Gly Ile Val Arg Lys Trp Ile Ser Arg Phe Glu Lys Val	
370 375 380	
tgg cca tac ttg gaa acc tac aca gag gat gtt gct cat gaa atc tcc	1200
Trp Pro Tyr Leu Glu Thr Tyr Thr Glu Asp Val Ala His Glu Ile Ser	
385 390 395 400	
aaa gag ttg cac ggc acg cca gat ctg atc atc gga aac nac agc gac	1248
Lys Glu Leu His Gly Thr Pro Asp Leu Ile Ile Gly Asn Xaa Ser Asp	
405 410 415	
ggc aat atc gtc gcc tcc ttg ctc gca cat aaa tta ggt gtc aca cag	1296
Gly Asn Ile Val Ala Ser Leu Leu Ala His Lys Leu Gly Val Thr Gln	
420 425 430	
ggc acc atc gcc cat gct ttg gag aag aca aaa tat cca gat tca gat	1344
Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser Asp	
435 440 445	
atc tat tgg aag aag ctt gaa gac aaa tac cat ttc tct tgc caa ttt	1392
Ile Tyr Trp Lys Lys Leu Glu Asp Lys Tyr His Phe Ser Cys Gln Phe	
450 455 460	
aca gct gat ctt ttt gca atg aac cat aca gat ttc atc atc acc agt	1440
Thr Ala Asp Leu Phe Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser	
465 470 475 480	
act ttc cag gaa att gca gga agc aag gac act gtt ggt caa tac gag	1488
Thr Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly Gln Tyr Glu	
485 490 495	
agc cac act gct ttc act ctt cct ggt ctc tac cgt gtt gta cat ggt	1536
Ser His Thr Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly	
500 505 510	
atc gat gtg ttt gat ccc aaa ttc aac att gtt tcc cct ggt gct gat	1584
Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp	
515 520 525	
atg gag ata tac ttc cct tac acc gaa gag aag cgg agg ttg aag cat	1632
Met Glu Ile Tyr Phe Pro Tyr Thr Glu Glu Lys Arg Arg Leu Lys His	
530 535 540	
ttc cat cct gag atc gaa gac ctt ctt tac acc aaa gtt gag aat gaa	1680
Phe His Pro Glu Ile Glu Asp Leu Leu Tyr Thr Lys Val Glu Asn Glu	

545		550		555		560										
gaa	cac	tta	tgt	gtg	ctc	aat	gac	cgc	aac	aag	cca	att	ctg	ttc	aca	1728
Glu	His	Leu	Cys	Val	Leu	Asn	Asp	Arg	Asn	Lys	Pro	Ile	Leu	Phe	Thr	
				565					570					575		
atg	cca	agg	ctt	gat	cgt	gtc	aag	aac	tta	acc	gga	ctc	gtc	gag	tgg	1776
Met	Pro	Arg	Leu	Asp	Arg	Val	Lys	Asn	Leu	Thr	Gly	Leu	Val	Glu	Trp	
			580					585					590			
tgc	ggc	aag	aac	cca	aag	ttg	cgt	gag	ttg	gct	aac	ctc	gta	gtt	gta	1824
Cys	Gly	Lys	Asn	Pro	Lys	Leu	Arg	Glu	Leu	Ala	Asn	Leu	Val	Val	Val	
		595					600					605				
ggt	ggt	gat	agg	cga	aag	gaa	tct	aaa	gat	ttg	gaa	gag	aag	gct	gaa	1872
Gly	Gly	Asp	Arg	Arg	Lys	Glu	Ser	Lys	Asp	Leu	Glu	Glu	Lys	Ala	Glu	
	610					615					620					
atg	aag	aaa	atg	ttt	gag	ctg	atc	gac	aag	tac	aac	ttg	aac	ggc	caa	1920
Met	Lys	Lys	Met	Phe	Glu	Leu	Ile	Asp	Lys	Tyr	Asn	Leu	Asn	Gly	Gln	
	625				630					635					640	
ctc	aga	tgg	ata	tca	tct	caa	atg	aac	aga	atc	cga	aat	gtt	gaa	ctt	1968
Phe	Arg	Trp	Ile	Ser	Ser	Gln	Met	Asn	Arg	Ile	Arg	Asn	Val	Glu	Leu	
				645					650					655		
tac	cga	tac	att	tgc	gac	acg	aaa	ggt	gcc	ttt	gta	cag	cct	gca	ttg	2016
Tyr	Arg	Tyr	Ile	Cys	Asp	Thr	Lys	Gly	Ala	Phe	Val	Gln	Pro	Ala	Leu	
			660					665					670			
tat	gaa	gcc	ttt	gga	ttg	aca	gtt	gtg	gag	gca	atg	act	tgc	ggc	ttg	2064
Tyr	Glu	Ala	Phe	Gly	Leu	Thr	Val	Val	Glu	Ala	Met	Thr	Cys	Gly	Leu	
		675					680					685				
cca	aca	ttc	gca	acc	tgt	aac	ggt	gga	cca	gcc	gag	att	att	gtc	cat	2112
Pro	Thr	Phe	Ala	Thr	Cys	Asn	Gly	Gly	Pro	Ala	Glu	Ile	Ile	Val	His	
	690					695					700					
ggg	aaa	tct	ggt	ttc	aac	att	gat	cct	tac	cat	ggt	gat	caa	gct	gct	2160
Gly	Lys	Ser	Gly	Phe	Asn	Ile	Asp	Pro	Tyr	His	Gly	Asp	Gln	Ala	Ala	
	705				710					715					720	
gac	ata	ctc	gtc	gat	ttc	ttt	gaa	aag	tgt	aag	aaa	gat	cca	tct	cac	2208
Asp	Ile	Leu	Val	Asp	Phe	Phe	Glu	Lys	Cys	Lys	Lys	Asp	Pro	Ser	His	
				725					730					735		
tgg	gat	aag	atc	tcc	caa	gga	ggc	ttg	aaa	cga	ata	gag	gag	aag	tat	2256
Trp	Asp	Lys	Ile	Ser	Gln	Gly	Gly	Leu	Lys	Arg	Ile	Glu	Glu	Lys	Tyr	
			740					745					750			
aca	tgg	aag	att	tac	tcg	gag	aga	cta	ttg	acc	ctg	aca	gga	gtg	tat	2304
Thr	Trp	Lys	Ile	Tyr	Ser	Glu	Arg	Leu	Leu	Thr	Leu	Thr	Gly	Val	Tyr	
		755					760					765				
gga	ttc	tgg	aag	cat	gtt	tcc	aac	ctt	gaa	cgc	cgt	gag	agt	cgt	cgt	2352
Gly	Phe	Trp	Lys	His	Val	Ser	Asn	Leu	Glu	Arg	Arg	Glu	Ser	Arg	Arg	
	770					775					780					

tac ctt gag atg ttt tat gct ctt aag tac cgt aag ctg gct gaa tca 2400
 Tyr Leu Glu Met Phe Tyr Ala Leu Lys Tyr Arg Lys Leu Ala Glu Ser
 785 790 795 800

ggt cca ttg gca gag gag taa att gaa cct gtt aaa taa cat tgg gcc 2448
 Val Pro Leu Ala Glu Glu Ile Glu Pro Val Lys His Trp Ala
 805 810

ggt ttt tct tgg aga ata ata ttc tgt ttt gta att tca att gga gaa 2496
 Gly Phe Ser Trp Arg Ile Ile Phe Cys Phe Val Ile Ser Ile Gly Glu
 815 820 825 830

gct cct ttg tat ttc atc ttg tct ttt cct ttt cct ttt ttc gcc ggc 2544
 Ala Pro Leu Tyr Phe Ile Leu Ser Phe Pro Phe Pro Phe Phe Ala Gly
 835 840 845

att gtt tga aca tgg ggt tgt gcg ccc gtc aat tcc agt taa ata tgg 2592
 Ile Val Thr Trp Gly Cys Ala Pro Val Asn Ser Ser Ile Trp
 850 855 860

tga ctt ttg ttt ttc aaa aaa aaa aaa aaa aaa 2625
 Leu Leu Phe Phe Lys Lys Lys Lys Lys Lys
 865 870

<210> 2
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 <212> PRT
 <213> Gossypium hirsutum

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 <222> (414)..(414)
 <223> The 'Xaa' at location 414 stands for Asn, Asp, His, or Tyr.

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Asp Glu Thr Leu Leu Ala His Arg Asn Glu Ile Leu Ala Leu Leu Ser
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Arg Ile Glu Gly Lys Gly Lys Gly Ile Leu Gln His His Gln Ile Ile
 35 40 45

Leu Glu Phe Glu Ala Ile Pro Glu Glu Asn Arg Lys Lys Leu Ala Asn
 50 55 60

Gly Ala Phe Phe Glu Val Leu Lys Ala Ser Gln Glu Ala Ile Val Leu
65 70 75 80

Pro Pro Trp Val Ala Leu Ala Val Arg Pro Arg Pro Gly Val Trp Glu
85 90 95

Tyr Ile Arg Val Asn Val His Ala Leu Val Val Glu Glu Leu Thr Val
100 105 110

Ala Glu Tyr Leu His Phe Lys Glu Glu Leu Val Asp Gly Ser Ser Asn
115 120 125

Gly Asn Phe Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ser Ser Phe
130 135 140

Pro Arg Pro Thr Leu Ser Lys Ser Ile Gly Asn Gly Val Glu Phe Leu
145 150 155 160

Asn Arg His Leu Ser Ala Lys Leu Phe His Asp Lys Glu Ser Met His
165 170 175

Pro Leu Leu Glu Phe Leu Arg Val His Cys His Lys Gly Lys Asn Met
180 185 190

Met Leu Asn Asp Arg Ile Gln Asn Leu Asn Ala Leu Gln His Val Leu
195 200 205

Arg Lys Ala Glu Glu Tyr Leu Gly Thr Leu Pro Pro Glu Thr Pro Cys
210 215 220

Ala Glu Phe Glu His Arg Phe Gln Glu Ile Gly Leu Glu Arg Gly Trp
225 230 235 240

Gly Asp Thr Ala Glu Arg Val Leu Glu Met Ile Gln Leu Leu Leu Asp
245 250 255

Leu Leu Glu Ala Thr Asp Pro Cys Thr Leu Glu Lys Phe Leu Gly Arg
260 265 270

Ile Pro Met Val Phe Asn Val Val Ile Leu Thr Pro His Gly Tyr Phe
275 280 285

Ala Gln Asp Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val
290 295 300

Tyr Ile Leu Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg
 305 310 315 320

Ile Lys Gln Gln Gly Leu Asn Ile Thr Pro Arg Ile Leu Ile Ile Thr
 325 330 335

Arg Leu Leu Pro Asp Ala Val Gly Thr Thr Cys Gly Gln Arg Leu Glu
 340 345 350

Lys Val Tyr Gly Thr Glu His Ser Asp Ile Leu Arg Val Pro Phe Arg
 355 360 365

Thr Glu Lys Gly Ile Val Arg Lys Trp Ile Ser Arg Phe Glu Lys Val
 370 375 380

Trp Pro Tyr Leu Glu Thr Tyr Thr Glu Asp Val Ala His Glu Ile Ser
 385 390 395 400

Lys Glu Leu His Gly Thr Pro Asp Leu Ile Ile Gly Asn Xaa Ser Asp
 405 410 415

Gly Asn Ile Val Ala Ser Leu Leu Ala His Lys Leu Gly Val Thr Gln
 420 425 430

Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser Asp
 435 440 445

Ile Tyr Trp Lys Lys Leu Glu Asp Lys Tyr His Phe Ser Cys Gln Phe
 450 455 460

Thr Ala Asp Leu Phe Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser
 465 470 475 480

Thr Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly Gln Tyr Glu
 485 490 495

Ser His Thr Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly
 500 505 510

Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp
 515 520 525

Met Glu Ile Tyr Phe Pro Tyr Thr Glu Glu Lys Arg Arg Leu Lys His
 530 535 540

Phe His Pro Glu Ile Glu Asp Leu Leu Tyr Thr Lys Val Glu Asn Glu
 545 550 555 560

Glu His Leu Cys Val Leu Asn Asp Arg Asn Lys Pro Ile Leu Phe Thr
 565 570 575

Met Pro Arg Leu Asp Arg Val Lys Asn Leu Thr Gly Leu Val Glu Trp
 580 585 590

Cys Gly Lys Asn Pro Lys Leu Arg Glu Leu Ala Asn Leu Val Val Val
 595 600 605

Gly Gly Asp Arg Arg Lys Glu Ser Lys Asp Leu Glu Glu Lys Ala Glu
 610 615 620

Met Lys Lys Met Phe Glu Leu Ile Asp Lys Tyr Asn Leu Asn Gly Gln
 625 630 635 640

Phe Arg Trp Ile Ser Ser Gln Met Asn Arg Ile Arg Asn Val Glu Leu
 645 650 655

Tyr Arg Tyr Ile Cys Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Leu
 660 665 670

Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu
 675 680 685

Pro Thr Phe Ala Thr Cys Asn Gly Gly Pro Ala Glu Ile Ile Val His
 690 695 700

Gly Lys Ser Gly Phe Asn Ile Asp Pro Tyr His Gly Asp Gln Ala Ala
 705 710 715 720

Asp Ile Leu Val Asp Phe Phe Glu Lys Cys Lys Lys Asp Pro Ser His
 725 730 735

Trp Asp Lys Ile Ser Gln Gly Gly Leu Lys Arg Ile Glu Glu Lys Tyr
 740 745 750

Thr Trp Lys Ile Tyr Ser Glu Arg Leu Leu Thr Leu Thr Gly Val Tyr
 755 760 765

Gly Phe Trp Lys His Val Ser Asn Leu Glu Arg Arg Glu Ser Arg Arg
 770 775 780

Tyr Leu Glu Met Phe Tyr Ala Leu Lys Tyr Arg Lys Leu Ala Glu Ser
 785 790 795 800

Val Pro Leu Ala Glu Glu
 805

<210> 3
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 <213> Gossypium hirsutum

<220>
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Ile Glu Pro Val Lys
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<210> 4
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His Trp Ala Gly Phe Ser Trp Arg Ile Ile Phe Cys Phe Val Ile Ser
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Ile Gly Glu Ala Pro Leu Tyr Phe Ile Leu Ser Phe Pro Phe Pro Phe
 20 25 30

Phe Ala Gly Ile Val
 35

<210> 5
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